BP 23: Biopolymers

Time: Thursday 10:00–13:00 Location: H43

Invited Talk BP 23.1 Thu 10:00 H43

Single-molecule Fluorescence Studies of RNA Folding and Function — •Gerd Ulrich Nienhaus — Institute of Applied Physics and Center for Functional Nanostructures, Karlsruhe Institute of Technology, 76128 Karlsruhe, Germany

RNA is a versatile biopolymer involved in various key biological functions, including storage and transfer of information, structural scaffolding and gene expression and regulation. RNA folds into compact three-dimensional structures, and RNA self-assembly and dynamics within the functionally competent, folded structure can be visualized by transitions in a highly complex energy landscape. We study these dynamic processes in small RNAs by using single-molecule Förster (fluorescence) resonance energy transfer (FRET). The free energies of the folded, intermediate and unfolded states can be changed by varying the Mg^{2+} counterion concentration, which allows one to selectively enhance the population of various states in thermal equilibrium and to analyze the equilibrium energetics as well as the kinetics and structural properties of these states.

BP 23.2 Thu 10:30 H43

(Un)folding of a high-temperature stable polyalanine helix from first principles — •Volker Blum, Mariana Rossi, Alex Tkatchenko, and Matthias Scheffler — Fritz-Haber-Institut der Max-Planck-Gesellschaft, D-14195 Berlin

Peptides *in vacuo* offer a unique, well-defined testbed to match experiments directly against first-principles approaches that predict the intramolecular interactions that govern peptide and protein folding. In this respect, the polyalanine-based peptide Ac-Ala_{15}-$LysH^+$ is particularly interesting, as it is experimentally known to form helices *in vacuo*, with stable secondary structure up to $\approx$ 750 K [1]. Room-temperature folding and unfolding timescales are usually not accessible by direct first-principles simulations, but this high T scale allows a rare direct first-principles view. We here use van der Waals corrected [2] density functional theory in the PBE generalized gradient approximation as implemented in the all-electron code FHI-aims [3] to show by Born-Oppenheimer *ab initio* molecular dynamics that Ac-Ala_{15}-$LysH^+$ indeed unfolds rapidly (within a few ps) at T=800 K and 1000 K, but not at 500 K. We show that the structural stability of the α helix at 500 K is critically linked to a correct van der Waals treatment, and that the designed $LysH^+$ ionic termination is essential for the observed helical secondary structure. [1] M. Kohtani *et al.*, JACS **126**, 7420 (2004). [2] A. Tkatchenko, M. Scheffler, PRL **102**, 073005 (2009). [3] V. Blum *et al.*, Comp. Phys. Comm. **180**, 2175 (2009).

BP 23.3 Thu 10:45 H43

Protein amyloid formation — •Chiu Fan Lee — Max Planck Institute for the Physics of Complex Systems Nöthnitzer Straße 38, 01187 Dresden, Germany

Protein amyloid fibrils are a form of linear protein aggregates that are implicated in many neurodegenerative diseases. Here, we study the equilibrium and dynamical properties of amyloid fibril formation. In particular, we discuss the length distribution of amyloid fibrils in thermal equilibrium [1], the possibility of isotropic-nematic phase transition as monomer concentration is increased [2], and the dynamical processes of nucleation and fibril elongation [3,4]. Our methods of investigation consist of techniques in statistical mechanics and molecular dynamics simulations.

References: [1] C.F. Lee (2009) Self-assembly of protein amyloid: a competition between amorphous and ordered aggregation. Physical Review E 80, 031922. [2] C.F. Lee (2009) Isotropic-nematic phase transition in amyloid fibrilization. Physical Review E 80, 031902. [3] L. Jean, C.F. Lee, C. Lee, M. Shaw and D.J. Vaux (2010) Competing discrete interfacial effects are critical for amyloidogenesis. To appear in the FASEB Journal. [4] C.F. Lee, J. Loken, L. Jean and D.J. Vaux (2009) Elongation dynamics of amyloid fibrils: a rugged energy landscape picture. Physical Review E 80, 041906.

BP 23.4 Thu 11:00 H43

Comparative analysis of rigidity across protein families — •Jose Emilio Jimenez, Stephen Wells, and Rudolf Römer — Department of Physics and Centre for Scientific Computing, University of Warwick, Coventry, CV4 7AL, UK

Protein rigidity analysis using the coarse graining FIRST/FRODA software package [1] has provided valuable insights in identifying the most flexible region of a protein [2]. Using the flexibility/rigidity restrictions given by FIRST/FRODA together with normal mode calculations makes it possible to simulate low frequency conformational changes in proteins at much lower computational cost than conventional molecular-dynamics methods.

Here we present a comparative study of rigidity across protein families that show two distinctive behaviors in their rigidity dilution patterns of proteins as hydrogen bonds are removed from weakest to strongest, one of sudden loss of rigidity and one of smooth transition [3]. This result highlights that choosing the energy cut off value should not be based on a numerical standard but chosen individually for each protein according to its rigidity pattern.

[1] S A Wells, et al, Constrained geometric simulation of diffusive motion in proteins. Physical Biology, 2, S127-S136, 2005 [2] D J Jacobs, et al. Protein flexibility predictions using graph theory. PROTEINS: Struct., Func. and Gen., 44:150*165, 2001. [3] S A Wells, J E Jimenez-Roldan and R A Römer. Comparative analysis of rigidity across protein families Phys. Biol. 6 046005, 2009

BP 23.5 Thu 11:15 H43

A Stevedore's Protein Knot — •Peter Virnau[1], Joanna Sulkowska[2], and Daniel Bölinger[3] — [1]Institut für Physik, Uni Mainz — [2]Center for Theoretical Biological Physics, UC San Diego, USA — [3]MPI für Neurobiologie, Martinsried

Protein knots, mostly regarded as intriguing oddities, are gradually being recognized as significant structural motifs. Seven distinctly knotted folds have already been identified. It is by and large unclear how these exceptional structures actually fold, and only recently, experiments and simulations have begun to shed some light on this issue. In checking the new protein structures submitted to the Protein Data Bank, we encountered the most complex, and the smallest, knots to date: A recently uncovered alpha-haloacid dehalogenase structure, contains a knot with six crossings, a so-called Stevedore knot, in a projection onto a plane. The smallest protein knot is present in an as yet unclassified protein fragment that consists of only 92 amino acids. The topological complexity of the Stevedore knot presents a puzzle as to how it could possibly fold. To unravel this enigma, we performed folding simulations with a structure-based coarse-grained model, and uncovered a possible mechanism by which the knot forms in a single loop flip.

15 min. break

BP 23.6 Thu 11:45 H43

Buckling and writhing of semiflexible polymer rings in confinement — •Katja Ostermeir, Karen Alim, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universtät München, Theresienstr. 37, D-80333 München

Cell walls or membranes impose a spatial confinement on semiflexible biopolymers such as DNA and cytoskeletal filaments. Restricting the accessible space changes a polymer's configurations and hence its properties in biological processes. Examining semiflexible polymers rings in spherical confinement we observe substantial transformations of polymers' shape and symmetry at relatively weak confinement.

While polymer rings with a small ratio of perimeter to persistence length would attain a planar, elliptical configuration in free space, we find that confinement forces them to buckle into banana-like shapes. We develop an analytical scaling argument which resolves a stiff polymer's shape for small flexibilities. Our calculation agrees with shape parameter measurements from Monte Carlo simulations over ranges of confinement.

More flexible free polymers rings tend to to take on prolate configurations which are again suppressed by the confinement. We discover an increased writhing of the polymer in order to store length without sharp bending. In the semiflexible regime a bimodal distribution of writhe is found.

BP 23.7 Thu 12:00 H43

Influence of filament positioning on polymerization of filament ensembles — •Jarosław Krawczyk and Jan Kier-

FELD — Technische Universität Dortmund, Lehrstuhl für Theoretische Physik I,

Many cellular processes are driven by polymerization of filamentous proteins. Using stochastic simulations based on the Gillespie algorithm we investigate force-generation by polymerizing groups of filaments or protofilaments and study the influence of the relative starting positions of filaments on the dynamics of growing speed. We find a strong influence of the starting position on the growth velocity. While the growth velocity for different starting configurations differ, the stall force remains unchanged.

BP 23.8 Thu 12:15 H43

Tube Width Fluctuations in F-Actin Solutions — •JENS GLASER[1], DIPANJAN CHAKRABORTY[1], KLAUS KROY[1], INKA LAUTER[2], MASASHI DEGAWA[2], NORBERT KIRCHGESSNER[2], BERND HOFFMANN[2], RUDOLF MERKEL[2], and MARGRET GIESEN[2] — [1]Institut für Theoretische Physik, PF 100920, 04009 Leipzig — [2]Insititut für Bio- und Nanosysteme, Biomechanik (IBN-4), Forschungszentrum Jülich, 52425 Jülich

Edwards' tube model provides a simple phenomenological description of the complicated topological constraints in entangled solutions of flexible polymers. Using scaling arguments, the idea was generalized to stiff polymers with a persistence length larger than the characteristic arclength between mutual collisions, which plays the role of the entanglement length in this context. Their large contour and persistence lengths have opened the possibility of direct microscopic visualizations of the tube by superimposing snapshots of a fluorescent test filament. We determine the statistics of the tube width in F-actin solutions, beyond the usually reported mean value [1]. The experimental observations are explained by a segment fluid description based on the binary collision approximation (BCA) [2]. In this systematic generalization of the standard mean-field approach, effective polymer segments ("entanglons") interact via a potential representing the topological constraints. The theory is complemented by Brownian dynamics and Monte Carlo simulations.

[1] J. Glaser et al., arXiv:0910.5864
[2] D.C. Morse, PRE 63:031502 (2001)

BP 23.9 Thu 12:30 H43

Intermediate filament assembly in micro-flow studied by X-ray scattering — •MARTHA BRENNICH, JENS NOLTING, CHRISTIAN DAMMANN, BERND NÖDING, SUSANNE BAUCH, and SARAH KÖSTER — Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany

The cytoskeleton, which is responsible for many mechanical properties of the cell, primarily consists of three different types of fibrous proteins: actin filaments, microtubules and intermediate filaments (IFs). The latter comprise a variety of proteins that vary from cell type to cell type. Our work is focused on the hierarchical self-assembly of IF subunits into filaments. We study these processes on the example of vimentin where the assembly can be initiated in vitro by increasing the salt concentration of the solution. Microfluidic tools are used to establish precise pH and salt concentration gradients, wherein the assembly occurs and can be observed in situ. Because of the small channel dimensions and the corresponding laminar flow, the time axis for the assembly process is projected onto a spatial axis along the flow direction and we observe different assembly states by collecting data at different positions in the device. A new type of 3D microfluidic device optimized for small angle X-ray scattering experiments allows us to obtain structural information on the first steps of the vimentin assembly. From the changes in the structural composition we deduce the kinetics of the filament formation and elongation.

BP 23.10 Thu 12:45 H43

Biomolecule Binding quantified with Thermophoresis — •CHRISTOPH J WIENKEN, PHILIPP BAASKE, DIETER BRAUN, and STEFAN DUHR — Systems Biophysics, Center for Nanoscience, LMU München, Germany

Methods to measure biomolecule interactions are essential for medicine, biology and pharmaceutical industry. We use thermophoresis, the directed movement of molecules in a temperature gradient, to quantify a wide range of interactions like protein protein, protein DNA and protein small molecule.

By combining highly defined microfluidics with all-optical heating and detection, the thermophoretically induced concentration change is measured with high precision. We fluorescently label one binder and track the changes of thermophoretic depletion while titrating the binding partner. The results are quantitative binding curves allowing to measure dissociation coefficients in the picomolar to milimolar range.

Advantages of the method are low volume consumption, fast response time and surface-free detection. However the measurement in various physiological buffers is the hallmark of the approach. Affinities can be measured in highly complex biological fluids as blood serum.

Thermophoresis is performed in bulk fluid, and significant background signals from surface binding are avoided. Competing surface-based methods such as ELISA or surface plasmon resonance have to measure on non-physiological surfaces that are prone to unspecific biomolecule adsorption and do not allow measurements in undiluted biological liquids.